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Application No: 10587372 Version No: 1.0

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<110> BAROJA FERNANDEZ, Miren Edurne
MUNOZ PEREZ, Francisco Jose
POZUETA ROMERO, Francisco Javier
MORAN ZORZANO, Maria Teresa
ALONSO CASAJUS, Nora

<120> METHOD OF PRODUCTION OF RECOMBINANT SUCROSE SYNTHASE, USE THEREOF IN THE MANUFACTURE OF KITS FOR DETERMINATION OF SUCROSE, PRODUCTION OF ADPGLUCOSE AND PRODUCTION OF TRANSGENIC PLANTS WHOSE LEAVES AND STORAGE ORGANS ACCUMULATE HIGH CONTENTS OF ADPGLUCOSE AND STARCH

<130> U 016405-8

<140> 10587372
<141> 2009-05-18

<160> 12

<170> PatentIn version 3.3

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<213> Solanum tuberosum

<220>
<223> Promoter of the 5' region of SS4

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<223> Promoter of the 3' region of SS4

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gaacttgtcg acggagcctc gaatggaaat tttgttctcg agttggattt cgagcctttc 420

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<211> 841
<212> PRT
<213> Solanum tuberosum

<220>
<223> SSX fused with a histidine-rich amino acid tail deducted after expression of SSX in the PET-28a(+) expression plasmid

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Gly Ser Glu Phe Met Ala Glu Arg Val Leu Thr Arg Val His Ser Leu
35 40 45

Arg Glu Arg Val Asp Ala Thr Leu Ala Ala His Arg Asn Glu Ile Leu
50 55 60

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Leu Phe Leu Ser Arg Ile Glu Ser His Gly Lys Gly Ile Leu Lys Pro
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His Glu Leu Leu Ala Glu Phe Asp Ala Ile Arg Gln Asp Asp Lys Asn
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Lys Leu Asn Glu His Ala Phe Glu Glu Leu Leu Lys Ser Thr Gln Glu
            100                 105                 110

Ala Ile Val Leu Pro Pro Trp Val Ala Leu Ala Ile Arg Leu Arg Pro
        115                 120                 125

Gly Val Trp Glu Tyr Ile Arg Val Asn Val Asn Ala Leu Val Val Glu
    130                 135                 140

Glu Leu Ser Val Pro Glu Tyr Leu Gln Phe Lys Glu Glu Leu Val Asp
145                 150                 155                 160

Gly Ala Ser Asn Gly Asn Phe Val Leu Glu Leu Asp Phe Glu Pro Phe
                165                 170                 175

Thr Ala Ser Phe Pro Lys Pro Thr Leu Thr Lys Ser Ile Gly Asn Gly
            180                 185                 190

Val Glu Phe Leu Asn Arg His Leu Ser Ala Lys Met Phe His Asp Lys
        195                 200                 205

Glu Ser Met Thr Pro Leu Leu Glu Phe Leu Arg Ala His His Tyr Lys
    210                 215                 220

Gly Lys Thr Met Met Leu Asn Asp Arg Ile Gln Asn Ser Asn Thr Leu
225                 230                 235                 240

Gln Asn Val Leu Arg Lys Ala Glu Glu Tyr Leu Ile Met Leu Ser Pro
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Asp Thr Pro Tyr Phe Glu Phe Glu His Lys Phe Gln Glu Ile Gly Leu
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Glu Lys Gly Trp Gly Asp Thr Ala Glu Arg Val Leu Glu Met Val Cys
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Met Leu Leu Asp Leu Leu Glu Ala Pro Asp Ser Cys Thr Leu Glu Lys
```

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Phe Leu Gly Arg Ile Pro Met Val Phe Asn Val Val Ile Leu Ser Pro
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His Gly Tyr Phe Ala Gln Glu Asn Val Leu Gly Tyr Pro Asp Thr Gly
                325                 330                 335

Gly Gln Val Val Tyr Ile Leu Asp Gln Val Pro Ala Leu Glu Arg Glu
            340                 345                 350

Met Leu Lys Arg Ile Lys Glu Gln Gly Leu Asp Ile Ile Pro Arg Ile
        355                 360                 365

Leu Ile Val Thr Arg Leu Leu Pro Asp Ala Val Gly Thr Thr Cys Gly
    370                 375                 380

Gln Arg Ile Glu Lys Val Tyr Gly Ala Glu His Ser His Ile Leu Arg
385                 390                 395                 400

Val Pro Phe Arg Thr Glu Lys Gly Ile Val Arg Lys Trp Ile Ser Arg
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Phe Glu Val Trp Pro Tyr Met Glu Thr Phe Ile Glu Asp Val Ala Lys
            420                 425                 430

Glu Ile Ser Ala Glu Leu Gln Ala Lys Pro Asp Leu Ile Ile Gly Asn
        435                 440                 445

Tyr Ser Glu Gly Asn Leu Ala Ala Ser Leu Leu Ala His Lys Leu Gly
    450                 455                 460

Val Thr Gln Cys Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro
465                 470                 475                 480

Asp Ser Asp Ile Tyr Trp Lys Lys Phe Asp Glu Lys Tyr His Phe Ser
                485                 490                 495

Ser Gln Phe Thr Ala Asp Leu Ile Ala Met Asn His Thr Asp Phe Ile
            500                 505                 510

Ile Thr Ser Thr Phe Gln Glu Ile Ala Gly Ser Lys Asp Thr Val Gly
        515                 520                 525
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```
Gln Tyr Glu Ser His Met Ala Phe Thr Met Pro Gly Leu Tyr Arg Val
    530                 535                 540

Val His Gly Ile Asn Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro
545                 550                 555                 560

Gly Ala Asp Ile Asn Leu Tyr Phe Ser Tyr Ser Glu Thr Glu Lys Arg
                565                 570                 575

Leu Thr Ala Phe His Pro Glu Ile Asp Glu Leu Leu Tyr Ser Asp Val
            580                 585                 590

Glu Asn Asp Glu His Leu Cys Val Leu Lys Asp Arg Thr Lys Pro Ile
        595                 600                 605

Leu Phe Thr Met Ala Arg Leu Asp Arg Val Lys Asn Leu Thr Gly Leu
    610                 615                 620

Val Glu Trp Tyr Ala Lys Asn Pro Arg Leu Arg Gly Leu Val Asn Leu
625                 630                 635                 640

Val Val Val Gly Gly Asp Arg Arg Lys Glu Ser Lys Asp Leu Glu Glu
                645                 650                 655

Gln Ala Glu Met Lys Lys Met Tyr Glu Leu Ile Glu Thr His Asn Leu
            660                 665                 670

Asn Gly Gln Phe Arg Trp Ile Ser Ser Gln Met Asn Arg Val Arg Asn
        675                 680                 685

Gly Glu Leu Tyr Arg Tyr Ile Ala Asp Thr Lys Gly Ala Phe Val Gln
    690                 695                 700

Pro Ala Phe Tyr Glu Ala Phe Gly Leu Thr Val Val Glu Ala Met Thr
705                 710                 715                 720

Cys Gly Leu Pro Thr Phe Ala Thr Asn His Gly Gly Pro Ala Glu Ile
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Ile Val His Gly Lys Ser Gly Phe His Ile Asp Pro Tyr His Gly Glu
            740                 745                 750
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Gln Ala Ala Asp Leu Leu Ala Asp Phe Phe Glu Lys Cys Lys Lys Glu
        755                 760                 765

Pro Ser His Trp Glu Thr Ile Ser Thr Gly Gly Leu Lys Arg Ile Gln
    770                 775                 780

Glu Lys Tyr Thr Trp Gln Ile Tyr Ser Glu Arg Leu Leu Thr Leu Ala
785                 790                 795                 800

Ala Val Tyr Gly Phe Trp Lys His Val Ser Lys Leu Asp Arg Leu Glu
                805                 810                 815

Ile Arg Arg Tyr Leu Glu Met Phe Tyr Ala Leu Lys Tyr Arg Lys Met
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Ala Glu Ala Val Pro Leu Ala Ala Glu
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<211> 41
<212> DNA
<213> Solanum tuberosum

<220>
<223> "Forward" promoter required for the point mutagenesis of SSX

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<210> 6
<211> 41
<212> DNA
<213> Solanum tuberosum

<220>
<223> "Reverse" promoter required for the point mutagenesis of SSX

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<210> 7
<211> 42
<212> DNA
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<220>
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<213> Solanum tuberosum

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<211> 76
<212> DNA
<213> Solanum tuberosum

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<223> "Forward" promoter required for point mutagenesis of SSX and production of SS5

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ctgaagcgca tccaag 76

<210> 10
<211> 76
<212> DNA
<213> Solanum tuberosum

<220>
<223> "Reverse" promoter required for point mutagenesis of SSX and production of SS5

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<212> DNA
<213> Solanum tuberosum

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atattgaaac ctcacgagct tttggctgag ttcgatgcaa ttcgccaaga tgacaaaaac   180

aaactgaacg aacatgcatt cgaagaaccc ctgaaatcca ctcaggaagc gattgttctg   240

ccccccttggg ttgcacttgc tattcgtttg aggcctggtg tctgggaata catccgtgtg   300

aacgtcaatg cactagttgt cgaggagctg tccgtccctg agtatttgca attcaaggaa   360

gaacttgtcg acggagcctc gaatggaaat ttcgttctcg agttggattt cgagcctttc   420

actgcatcct ttcctaaacc aaccctcacc aaatctattg gaaatggagt tgaattcctc   480

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gatactccat atttcgaatt cgagcacaag ttccaagaaa tcggattgga gaagggatgg   720

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<210> 12
<211> 841
<212> PRT
<213> Solanum tuberosum

<220>
<223> SS5 fused with a histidine-rich amino acid sequence

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1 5 10 15

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
20 25 30

Gly Ser Glu Phe Met Ala Glu Arg Val Leu Thr Arg Val His Ser Leu
35 40 45

Arg Glu Arg Val Asp Ala Thr Leu Ala Ala His Arg Asn Glu Ile Leu
50 55 60

```
Leu Phe Leu Ser Arg Ile Glu Ser His Gly Lys Gly Ile Leu Lys Pro
65                  70                  75                  80

His Glu Leu Leu Ala Glu Phe Asp Ala Ile Arg Gln Asp Asp Lys Asn
                85                  90                  95

Lys Leu Asn Glu His Ala Phe Glu Glu Pro Leu Lys Ser Thr Gln Glu
            100                 105                 110

Ala Ile Val Leu Pro Pro Trp Val Ala Leu Ala Ile Arg Leu Arg Pro
        115                 120                 125

Gly Val Trp Glu Tyr Ile Arg Val Asn Val Asn Ala Leu Val Val Glu
    130                 135                 140

Glu Leu Ser Val Pro Glu Tyr Leu Gln Phe Lys Glu Glu Leu Val Asp
145                 150                 155                 160

Gly Ala Ser Asn Gly Asn Phe Val Leu Glu Leu Asp Phe Glu Pro Phe
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